

IN THE CLAIMS

Please amend the following claims without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents:

D 1
C 1
~~1. (Twice Amended) A chaperone polypeptide having an amino acid sequence selected from at least amino acid residues 230-271 but no more than residues 150-455 or 151-456 of a GroEL sequence as shown in Figure 7, or a corresponding sequence of a chaperone polypeptide, said corresponding sequence sharing at least 50% homology with said amino acid sequence.~~

~~12. (Twice Amended) A polypeptide as claimed in claim 1 which comprises at least an amino acid sequence selected from GroEL residues:~~

- (a) 191-329, 191-330, 191-331, 191-332, 191-333, 191-334, 191-335, 191-336, 191-337, 191-338, 191-339, 191-340, 191-341, 191-342, 191-343, 191-344, 191-345, 191-346, 191-347, 191-348, 191-349, 191-350, 191-351, 191-352, 191-353, 191-354, 191-355, 191-356, 191-357, 191-358, 191-359, 191-360, 191-361, 191-362, 191-363, 191-364, 191-365, 191-366, 191-367, 191-368, 191-369, 191-370, 191-371, 191-372, 191-373, 191-374, 191-375 or 191-376, or
- (b) 192-329, 192-330, 192-331, 192-332, 192-333, 192-334, 192-335, 192-336, 192-337, 192-338, 192-339, 192-340, 192-341, 192-342, 192-343, 192-344, 192-345, 192-346, 192-347, 192-348, 192-349, 192-350, 192-351, 192-352, 192-353, 192-354, 192-355, 192-356, 192-357, 192-358, 192-359, 192-360, 192-361, 192-362, 192-363, 192-364, 192-365, 192-366, 192-367, 192-368, 192-369, 192-370, 192-371, 192-372, 192-373, 192-374, 192-375 or 192-376, or
- (c) 193-329, 193-330, 193-331, 193-332, 193-333, 193-334, 193-335, 193-336, 193-337, 193-338, 193-339, 193-340, 193-341, 193-342, 193-343, 193-344, 193-345, 193-346, 193-347, 193-348, 193-349, 193-350, 193-351, 193-352, 193-353, 193-354, 193-355, 193-356, 193-357, 193-358, 193-359, 193-360, 193-361, 193-362, 193-363, 193-364, 193-365, 193-366, 193-367, 193-368, 193-369, 193-370, 193-371, 193-372, 193-373, 193-374, 193-375 or 193-376, or
- (d) 230-271, 229-271, 229-272, 228-272, 228-273, ...et seq... 194-328, 194-329, or a corresponding sequence of a chaperone polypeptide, said corresponding sequence sharing at least 50% homology with said amino acid sequence.

6b
02

13. (Amended) A monomeric polypeptide, having chaperone activity and incapable of multimerisation, characterised in that, in the absence of ATP, the polypeptide has a protein refolding activity of more than 50%, said refolding activity being determined by contacting the polypeptide with an inactivated protein of known specific activity prior to inactivation, and then determining the specific activity of the said protein after contact with the polypeptide, the % refolding activity being:

$$\frac{\text{specific activity of protein after contact with polypeptide} \times 100}{\text{specific activity of protein prior to inactivation}} \quad 1$$

wherein the selected amino acid sequence is selected from the group consisting of 230-271, 191-345, 191-376, 193-335 and 193-337 of GroEL, or a corresponding sequence of a chaperone polypeptide, said corresponding sequence sharing at least 50% homology with said amino acid sequence.

Please add the following claims:

51. (New) A chaperone polypeptide having an amino acid sequence selected from at least amino acid residues 230-271, but no more than residues 150-455 or 151-456 of a GroEL sequence as shown in Figure 7, or a corresponding sequence of an hsp chaperonin protein selected from the group consisting of:

C 3

190-374 CH60_ECOLI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(AMS);
ESCHERICHIA 190-374 CH60_SALTI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); SALMONELLA TYPHI 191-375 S56371 GroEL protein; Escherichia coli 190-374 CH60_LEPIN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK 58 KD PRO 191-375 S47530 groEL protein); Porphyromonas gingivalis 190-374 LPNHTPBG LPNHTPBG NID:g149691; Legionella pneumophila (strain SVir) library: 189-373 CH60_ACTAC 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); ACTINOBACILLUS ACT 191-375 JC4519 heat-shock protein GroEL; Pasteurella multocida 191-375 CH60_BRUAB 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); BRUCELLA ABORTUS 191-375 CH60_HAEIN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); HAEMOPHILUS INFLUE 190-373 CH60_CAUCR 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CAULOBACTER CRESCE 190-374 CH60_AMOPS 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); AMOEBA PROTEUS SYM 191-375 CH60_HAEDU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); HAEMOPHILUS DUCREY 191-375 CH61_RHIME 60 KD CHAPERONIN A

(PROTEIN CPN60 A)(GROEL PROTEIN A); RHIZOBIUM ME 190-374 CH60_LEGMI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(58 KD COMMON ANTIGEN) 191-375 CH60_YEREN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK PROTEIN 6) 190-374 CH 63_BRAJA 60 KD CHAPERONIN 3 (PROTEIN CPN60 3)(GROEL PROTEIN 3); BRADYRHIZOBI 191-375 CH60_PORGI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); PORPHYROMONAS GING 191-375 S52901 heat shock protein 60K; Yersinia enterocolitica 191-375 S26423 heat shock protein 60; Yersinia enterocolitica 191-375 RSU373691 RSU37369 NID: g1208541; Rhodobacter sphaeroides strain=HR 190-374 CH62_BRAJA 60 KD CHAPERONIN 2 (PROTEIN CPN60 2)(GROEL PROTEIN 2); BRADYRHIZOBI 191-375 CH60_ACYPS 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(SYMBIONIN); ACYRTH 191-375 CH63_RHIME 60 KD CHAPERONIN C (PROTEIN CPN60 C)(GROEL PROTEIN C); RHIZOBIUM ME 191-375 YEPHSPCRP1 YEPHSPCRP NID: g466575; Yersinia enterocolitica DNA. 191-375 CH60_BORPE 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); BORDETELLA PERTUSS 189-373 BRUGRO1 BRUGRO NID: g144106; Brucella abortus (library: lambda-2001) DNA 191-375 CH60_PSEAE 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); PSEUDOMONAS AERUGI 190-374 CH60_BARBA 60 KD CHAPERONIN (PROTEIN CPN60)(IMMUNOREACTIVE PROTEIN BB65)(IMMUNO 191-375 BA0BB63A BA0BB63A) NID: g143845; Bartonella bacilliformis (library: ATCC 35685) 189-373 CH60_BACST 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); BACILLUS STEAROTHE 188-372 190-373 CH60_BORBU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); BORRELLIA BURGDORFE 224-408 S26583 chaperonin hsp60; maize 190-373 A49209 heat shock protein HSP60; Lyme disease spirochete 224-408 MZECPN60B MZECPN60B NID: g309558; Zea mays (strain B73)(library: Dash1 of P.S) 189-373 CH60_THEP3 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK 61 KD) PRO 188-372 CH60_STAEP 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK PROTEIN 6) 189-373 CH60_LACLA 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); LACTOCOCCUS LACTIS 188-374 CH61_STRAL 60 KD CHAPERONIN 1 (PROTEIN CPN60 1)(GROEL PROTEIN 1)(HSP58); STRE 191-375 CH60_CHLPN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CHLAMYDIA PNEUMONI 224-408 MZECPN60A MZECPN60A NID: g309556;

Zea mays (strain B73)(library:Dach ll of P) 190-373 HECHSPAB1 HECHSPAB NID: g712829; Helicobacter pylori (individual_isolate 85P) D 221-405 CH60_ARATH MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR; ARABIDOPSIS THALIANA (MOUS 224-408) CH60 ; MAIZE MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR; ZEA MAYS (MAIZE) 190-374 CH60_CHLTR 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(57 KD CHLAMYDIAL HYP) 189-373 CH60_STAAU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK PROTEIN 6) 189-373 CH60_CLOPE 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CLOSTRIDIUM PERFR 212-397 HS60; YEAST HEAT SHOCK PROTEIN 60 PRECURSOR (STIMULATOR FACTOR 1 66 KD COMPONENT) 217-403 CH60_PYRSA 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); PYRENOMONAS SALINA 191-377 CH60_EHRCH 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); EHRLICHIA CHAFFEEN 191-375 CHTGROE1 CHTGROE NID: g144503; C.trachomatis DNA. 188-372 CH60_THETH 60 KD CHAPERONIN(PROTEIN CPN60)(GROEL PROTEIN); THERMUS AQUATICUS 189-373 TAU294831 TAU29483 NID: g1122940; Thermus aquaticus. 190-378 CH60_RJCTS 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(MAJOR ANTIGEN 58)(5 189-375 SYCCPNC) SYCCPNC NID: g1001102; Synechocystis sp. (strain PCC6803,) DNA; 190-373 CPU308211 CPU30821 NID: g1016083; Cyanophora paradoxa. 189-373 CH61_MYCLE 60 KD CHAPERONIN 1 (PROTEIN CPN60 1)(GROEL PROTEIN 1); MYCOBACTERIU 239-423 PSU21139 PSU21139 NID: g806807; pea 191-377 CH60_COWRU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); COWDRIA RUMINANTI 245-429 RUBB_BRANA RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERON) 144-328 SCCPN60 SCCPN60 NID: g1167857; rye 153-338 CH60_EHRR1 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(55 KD MAJOR ANTIGEN) 245-429 RUBB_ARATH RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERON 235-419 ATU49357 ATU49357 NID: g1223909; thale cress strain=ecotype Wassilewskija 195-379 RUB1_BRANA RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA) 189-374 CH62_SYN13 60 KD CHAPERONIN 2 (PROTEIN CPN60 2)(GROEL HOMOLOG 2); SYNECHOCYSTI 178-362 RUBA_RICCO RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA) 190-375 CH60_ODOSI 60 KD

CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); ODONTELLA SINENSIS 236-420
PSU21105 PSU21105 NID: g1185389; pea. 224-409 CH60_BRANA MITOCHONDRIAL
CHAPERONIN CH60_BACSU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL
PROTEIN); BACILLUS SUBTILIS 191-375 CH60_AGRTU 60 KD CHAPERONIN
(PROTEIN CPN60)(GROEL PROTEIN); AGROBACTERIUM TUME 191-375 b36917 heat
shock protein GroEL; Agrobacterium tumefaciens 191-375 PAU17072 PAU17072 NID:
g576778; Pseudomonas aeruginosa. 191-375 CH60_RHILV 60 KD CHAPERONIN (PROTEIN
CPN60)(GROEL PROTEIN); RHIZOBIUM LEGUMINO 187-373 CH61_STRCO 60 KD
CHAPERONIN 1 (PROTEIN CPN60 1)(GROEL PROTEIN 1)(HSP58); STRE 191-375
CH60_COXBU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT
SHOCK PROTEIN B) 191-375 CH62_RHIME 60 KD CHAPERONIN B (PROTEIN CPN60
B)(GROEL PROTEIN B); RHIZOBIUM ME 191-375 PSEGROESL1 PSEGROESL NID:
g151241; Pseudomonas aeruginosa (library: ATCC 27853) 189-372 CH61_SYNY3 60 KD
CHAPERONIN 1 (PROTEIN CPN60 1)(GROEL HOMOLOG 1).-SYNECHOCYSTI 189-373
CH60_CLOTM 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HSP-60);
CLOSTRIDI 191-373 CH60_PSEPU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL
PROTEIN); PSEUDOMONAS PUTIDA 190-373 CH60_SYNP7 60 KD CHAPERONIN
(PROTEIN CPN60)(GROEL PROTEIN); SYNECHOCOCCUS SP 190-374 CH60_GALSU 60
KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); GALDIERIA SULPHURA 190-
374 CH60_ZYMMO 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN);
ZYMO MONAS MOBILIS. 191-375 JC2564 heat shock protein groEL; Zymomonas mobilis
191-375 CH60_CHRVI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN);
CHROMATIUM VINO SUM 189-373 CH60_MYCTU 60 KD CHAPERONIN (PROTEIN
CPN60)(GROEL PROTEIN)(65 KD ANTIGEN)HEAT 191-375 CH60_NEIME 60 KD
CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(63 KD STRESS PROTEIN 189-373
CH60_TREPA 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(TPN60)(TP4
ANTIGEN) 190-374 CH60_HELPY 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL
PROTEIN)(HEAT SHOCK PROTEIN 6 191-375 CH60_NEIGO 60 KD CHAPERONIN
(PROTEIN CPN60)(GROEL PROTEIN)(63 KD STRESS PROTEIN) 222-406 CH61_CUCMA
MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR; CUCURBITA MAXIMA
(PUMPKI 189-373 CH60_MYCPA 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL

PROTEIN)(65 KD ANTIGEN)HEAT 230-414 MPU15989 MPU15989 NID:g559802; Mycobacterium paratuberculosis 224-408 S26582 chaperonin hsp60; maize 191-375 S40247 heat-shock protein; Neisseria gonorrhoeae 189-373 CH60_CLOAB 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CLOSTRIDIUM ACETOB 191-375 CH60_NEIFL 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(63 KD STRESS PROTEIN 190-373 CH60_LEGPN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(58 KD COMMON ANTIGEN) 222-406 CH62_CUCMA MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR; CUCURBITA MAXIMA (PUMPKI 191-375 CHTGROESL1 CHTGROESL NID: g402332; Chlamydia trachomatis DNA 64-248 S40172 S40172 NID: g251679; Chlamydia psittaci pigeon strain P-1041 189-373 SYOGROEL2 SYOGROEL2 NID:g562270; Synechococcus vulgaris DNA 191-375 CH60_CHLPS 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(57 KD CHLAMYDIAL HYP) 188-372 CH62_STRAL 60 KD CHAPERONIN 2 (PROTEIN CPN60 2)(GROEL PROTEIN 2)(HSP56); STRE 189-373 CH62_MYCLE 60 KD CHAPERONIN 2 (PROTEIN CPN60 2)(GROEL PROTEIN 2)(65 KD ANTIGEN) 236-420 MSGANTM MSGANTM NID: g149923; M.leprae DNA, clone Y3178 CPN60 PRECURSOR; BRASSICA NAPUS (RAPE) 105-289 PMSARG2 PMSARG2 NID: g607157; Prochlorococcus marinus 234-417 RUB2_BRANA RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERO 75-259 CRECPN1A CRECPN1A NID: g603910; Chlamydomonas reinhardtii cDNA to mRNA 215-400 P60_CRIGR MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)(CH224-408 CRECPN1B CRECPN1B NID: g603912; Chlamydomonas reinhardtii cDNA to mRNA 191-375 RUBA_WHEAT RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERO 189-373 B47292 heat shock protein groEL; Mycobacterium tuberculosis 206-391 CELHSP60CP CELHSP60CP NID: g533166; Caenorhabditis elegans (strain CB1392) cDNA 215-400 P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)(CH 215-400 P60_MOUSE MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)(CH 215-400 P60_RAT MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)(CH 215-400 A41931) chaperonin hsp60; mouse 197-382 MMHSP60A MMHSP60A NID:g51451; house mouse 218-402 CH63_HELV 63 KD CHAPERONIN PRECURSOR (P63); HELIOTHIS VIRESSENS (NOCTUID MOTH)

205-390 EGHSP60GN EGHSP60GN NID: g1217625; Euglena gracilis. 222-407 HS60_SCHPO PROBABLE HEAT SHOCK PROTEIN 60 PRECURSOR; SCHIZOSACCHAROMYCES POMBE 198-385 S61295 heat shock protein 60; Trypanosoma cruzi 198-385 TRBMTHSP TRBMTHSP NID: g903883; Mitochondrion Trypanosoma brucei (strain EATRO 8-69 ECOGROELA ECOGROELA NID: g146268; E.coli DNA, clone E. 142-325 ENHCPN60P ENHCPN60P NID: g675513; Entamoeba histolytica (strain HM-1:IMSS) DNA 257-433 CH60_PLAFG MITOCHONDRIAL CHAPERONIN CPN60 PRECURSOR; PLASMODIUM FALCIPARUM (ISO 1-90 CRECPN1C CRECPN1C NID: g603914; Chlamydomonas reinhardtii cDNA to mRNA; 5-65 ATTS0779 ATTS0779 NID: g17503; thale cress 189-373 CH60_MYCGE 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); MYCOPLASMA GENITAL 228-411 HTOHSP60X HTOHSP60X NID: g553068; Histoplasma capsulatum (strain G217B) DNA 190-297 CH60_SYN6 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(FRAGMENT); and SYNECHO 169-245 RUBA_ARATH RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA).

52. (New) A chaperone polypeptide having an amino acid sequence selected from at least amino acid residues 230-271 but no more than residues 150-455 or 151-456 of a GroEL sequence as shown in Figure 7, or a corresponding sequence of a chaperonin protein selected from the group consisting of:

CH60_ECOLI_190; CH60_SALTI_190; S56371_191; CH60_LEPIN_190; S47530_191; LPNHTPBG_190; CH60_ACTAC_189; JC4519_191; CH60_BRUAB_191; CH60_HAEIN_191; CH60_CAUCR_190; CH60_AMOPS_190; CH60_HAEDU_191; CH61_RHIME_191; CH60_LEGMI_190; CH60_YEREN_191; CH63_BRAJA_190; CH60_PORGI_191; S52901_191; S26423_191; RSU373691_191; CH62_BRAJA_190; CH60_ACYPS_191; CH63_RHIME_191; YEPHSPCRP1_191; CH60_BORPE_191; BRUGRO1_189; CH60_PSEAE_191; CH60_BARBA_190; BAOBB63A_191; CH60_BACST_189; CH60_BACSU_188; CH60_AGRTU_191; B36917_191; PAU17072_191; CH60_RHILV_191; CH61_STRCO_187; CH60_COXBU_191; CH62_RHIME_191; PSEGROESL1_191; CH61_SYN6_189; CH60_CLOTM_189; CH60_PSEPU_191; CH60_SYN7_190; CH60_GALSU_190; CH60_ZYMMO_190; JC2564_191; CH60_CHRVI_191; CH60_MYCTU_189; CH60_NEIME_191; CH60_TREPA_189;

CH60_HELPY_190; CH60_NEIGO_191; CH61_CUCMA_222; CH60_MYCPA_189;
MPU15989_230 ; S26582_224 ; S40247_191 ; CH60_CLOAB_189; CH60_NEIFL_191;
CH60_LEGPN_190; CH62_CUCMA_222; CHTGROESL1_191; S40172_64 ;
SYOGROEL2_189 ; CH60_CHLPS_191; CH62_STRAL_188; CH62_MYCLE_189;
MSGANTM_236; CH60_BORBU_190; S26583_224; A49209_190; MZECPN60B_224;
CH60_THEP3_189; CH60_STAEP_188; CH60_LACLA_189; CH61_STRAL_188;
CH60_CHLPN_191; MZECPN60A_224; HECHSPAB1_190; CH60_ARATH_221;
CH60_MAIZE_224; CH60_CHLTR_190; CH60_STAAU_189; CH60_CLOPE_189;
HS60_YEAST_212; CH60_PYRSA_217; CH60_EHRCH_191; CHTGROE1_191;
CH60_THETH_188; TAU294831_189; CH60_RICTS_190; SYCCPNC_189; CPU308211_190;
CH61_MYCLE_189; PSU21139_239; CH60_COWRU_191; RUBB_BRANA_245;
SCCPN60_144; CH60_EHRR1_153; RUBB_ARATH_245; ATU49357_235;
RUB1_BRANA_195; CH62_SYN3_189; RUBA_RICCO_178; CH60_ODOSI_190;
PSU21105_236; CH60_BRANA_224; PMSARG2_105; RUB2_BRANA_234; CRECPN1A_75;
P60_CRIGR_215; CRECPN1B_224; RUBA_WHEAT_191; B47292_189; CELHSP60CP_206;
P60_HUMAN_215; P60_MOUSE_215; P60_RAT_215; A41931_215; MMHSP60A_197;
CH63_HELVI_218; EGHSP60GN_205; HS60_SCHPO_222; S61295_198; TRBMTHSP_198;
ENHCPN60P_142; CH60_PLAFG_257; CH60_MYCGE_189; and HTOHSP60X_228.

53. (New) A monomeric polypeptide having chaperone activity and incapable of multimerisation characterised in that in the absence of ATP the polypeptide has a protein refolding activity of more than 50%, said refolding activity being determined by contacting the polypeptide with an inactivated protein of known specific activity prior to inactivation, and then determining the specific activity of the said protein after contact with the polypeptide, the % refolding activity being:

$$\frac{\text{specific activity of protein after contact with polypeptide} \times 100}{\text{specific activity of protein prior to inactivation}} \quad 1$$

wherein the selected amino acid is selected from the group consisting of 230-271, 191-345, 191-376, 193-335 and 193-337 of GroEL and a corresponding sequence of an hsp chaperonin protein selected from the group consisting of:

190-374 CH60_ECOLI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(AMS);
ESCHERICHIA 190-374 CH60_SALTI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL

PROTEIN); SALMONELLA TYPHI 191-375 S56371 GroEL protein; Escherichia coli 190-374 CH60_LEPIN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK 58 KD PRO 191-375 S47530 groEL protein); Porphyromonas gingivalis 190-374 LPNHTPBG LPNHTPBG NID:g149691; Legionella pneumophila (strain SVir) library: 189-373 CH60_ACTAC 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); ACTINOBACILLUS ACT 191-375 JC4519 heat-shock protein GroEL; Pasteurella multocida 191-375 CH60_BRUAB 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); BRUCELLA ABORTUS 191-375 CH60_HAEIN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); HAEMOPHILUS INFLUE 190-373 CH60_CAUCR 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CAULOBACTER CRESCE 190-374 CH60_AMOPS 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); AMOEBA PROTEUS SYM 191-375 CH60_HAEDU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); HAEMOPHILUS DUCREY 191-375 CH61_RHIME 60 KD CHAPERONIN A (PROTEIN CPN60 A)(GROEL PROTEIN A); RHIZOBIUM ME 190-374 CH60_LEGMI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(58 KD COMMON ANTIGEN) 191-375 CH60_YEREN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK PROTEIN 6) 190-374 CH 63_BRAJA 60 KD CHAPERONIN 3 (PROTEIN CPN60 3)(GROEL PROTEIN 3); BRADYRHIZOBI 191-375 CH60_PORGI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); PORPHYROMONAS GING 191-375 S52901 heat shock protein 60K; Yersinia enterocolitica 191-375 S26423 heat shock protein 60; Yersinia enterocolitica 191-375 RSU373691 RSU37369 NID: g1208541; Rhodobacter sphaeroides strain=HR 190-374 CH62_BRAJA 60 KD CHAPERONIN 2 (PROTEIN CPN60 2)(GROEL PROTEIN 2); BRADYRHIZOBI 191-375 CH60_ACYPS 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(SYMBIONIN); ACYRTH 191-375 CH63_RHIME 60 KD CHAPERONIN C (PROTEIN CPN60 C)(GROEL PROTEIN C); RHIZOBIUM ME 191-375 YEPHSPCRP1 YEPHSPCRP NID: g466575; Yersinia enterocolitica DNA. 191-375 CH60_BORPE 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); BORDETELLA PERTUSS 189-373 BRUGRO1 BRUGRO NID: g144106; Brucella aabortus (library: lambda-2001) DNA 191-375 CH60_PSEAE 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); PSEUDOMONAS AERUGI 190-374 CH60_BARBA 60 KD CHAPERONIN (PROTEIN CPN60)(IMMUNOREACTIVE PROTEIN BB65)(IMMUNO 191-

375 BAOBB63A BAOBB63A NID: g143845; Bartonella bacilliformis (library: ATCC 35685) 189-373 CH60_BACST 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); BACILLUS STEAROTHE 188-372 190-373 CH60_BORBU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); BORRELIA BURGDORFE 224-408 S26583 chaperonin hsp60; maize 190-373 A49209 heat shock protein HSP60; Lyme disease spirochete 224-408 MZECPN60B MZECPN60B NID: g309558; Zea mays (strain B73)(library:Dashll of P.S) 189-373 CH60_THEP3 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK 61 KD) PRO 188-372 CH60_STAEP 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK PROTEIN 6) 189-373 CH60_LACLA 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); LACTOCOCCUS LACTIS 188-374 CH61_STRAL 60 KD CHAPERONIN 1 (PROTEIN CPN60 1)(GROEL PROTEIN 1)(HSP58); STRE 191-375 CH60_CHLPN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CHLAMYDIA PNEUMONI 224-408 MZECPN60A MZECPN60A NID: g309556; Zea mays (strain B73)(library:Dach ll of P) 190-373 HECHSPAB1 HECHSPAB NID: g712829; Helicobacter pylori (individual_isolate 85P) D 221-405 CH60_ARATH MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR; ARABIDOPSIS THALIANA (MOUS 224-408) CH60_MAIZE MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR; ZEA MAYS (MAIZE) 190-374 CH60_CHLTR 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(57 KD CHLAMYDIAL HYP) 189-373 CH60_STAAU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK PROTEIN 6) 189-373 CH60_CLOPE 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CLOSTRIDIUM PERFRI 212-397 HS60; YEAST HEAT SHOCK PROTEIN 60 PRECURSOR (STIMULATOR FACTOR 1 66 KD COMPONENT) 217-403 CH60_PYRSA 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); PYRENOMONAS SALINA 191-377 CH60_EHRCH 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); EHRLICHIA CHAFFEEN 191-375 CHTGROE1 CHTGROE NID: g144503; C.trachomatis DNA. 188-372 CH60_THETH 60 KD CHAPERONIN(PROTEIN CPN60)(GROEL PROTEIN); THERMUS AQUATICUS 189-373 TAU294831 TAU29483 NID: g1122940; Thermus aquaticus. 190-378 CH60_RICTS 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(MAJOR ANTIGEN 58)(5 189-375 SYCCPNC) SYCCPNC NID: g1001102; Synechocystis sp. (strain PCC6803,) DNA; 190-373 CPU308211 CPU30821 NID: g1016083; Cyanophora paradoxa. 189-373 CH61_MYCLE 60 KD

CHAPERONIN 1 (PROTEIN CPN60 1)(GROEL PROTEIN 1); MYCOBACTERIUM 239-423
PSU21139 PSU21139 NID: g806807; pea 191-377 CH60_COWRU 60 KD CHAPERONIN
(PROTEIN CPN60)(GROEL PROTEIN); COWDRIA RUMINANTI 245-429
RUBB_BRANA RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR
(60 KD CHAPERON) 144-328 SCCPN60 SCCPN60 NID: g1167857; rye 153-338
CH60_EHRR 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(55 KD MAJOR
ANTIGEN) 245-429 RUBB_ARATH RUBISCO SUBUNIT BINDING-PROTEIN BETA
SUBUNIT PRECURSOR (60 KD CHAPERON 235-419 ATU49357 ATU49357 NID:
g1223909; thale cress strain=ecotype Wassilewskija 195-379 RUB1_BRANA RUBISCO
SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA) 189-374
CH62_SYN 60 KD CHAPERONIN 2 (PROTEIN CPN60 2)(GROEL HOMOLOG 2);
SYNECHOCYSTI 178-362 RUBA_RICCO RUBISCO SUBUNIT BINDING-PROTEIN
ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA) 190-375 CH60_ODOSI 60 KD
CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); ODONTELLA SINENSIS 236-420
PSU21105 PSU21105 NID: g1185389; pea. 224-409 CH60_BRANA MITOCHONDRIAL
CHAPERONIN CH60_BACSU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL
PROTEIN); BACILLUS SUBTILIS 191-375 CH60_AGR 60 KD CHAPERONIN
(PROTEIN CPN60)(GROEL PROTEIN); AGROBACTERIUM TUME 191-375 b36917 heat
shock protein GroEL; Agrobacterium tumefaciens 191-375 PAU17072 PAU17072 NID:
g576778; Pseudomonas aeruginosa. 191-375 CH60_RHILV 60 KD CHAPERONIN (PROTEIN
CPN60)(GROEL PROTEIN); RHIZOBIUM LEGUMINO 187-373 CH61_STRCO 60 KD
CHAPERONIN 1 (PROTEIN CPN60 1)(GROEL PROTEIN 1)(HSP58); STRE 191-375
CH60_COXBU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT
SHOCK PROTEIN B) 191-375 CH62_RHIME 60 KD CHAPERONIN B (PROTEIN CPN60
B)(GROEL PROTEIN B); RHIZOBIUM ME 191-375 PSEGROESL1 PSEGROESL NID:
g151241; Pseudomonas aeruginosa (library: ATCC 27853) 189-372 CH61_SYN 60 KD
CHAPERONIN 1 (PROTEIN CPN60 1)(GROEL HOMOLOG 1).-SYNECHOCYSTI 189-373
CH60_CLOTM 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HSP-60);
CLOSTRIDI 191-373 CH60_PSEPU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL
PROTEIN); PSEUDOMONAS PUTIDA 190-373 CH60_SYN 60 KD CHAPERONIN
(PROTEIN CPN60)(GROEL PROTEIN); SYNECHOCOCCUS SP 190-374 CH60_GALSU 60

KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); GALDIERIA SULPHURA 190-374 CH60_ZYMMO 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); ZYMO MONAS MOBILIS 191-375 JC2564 heat shock protein groEL; Zymomonas mobilis 191-375 CH60_CHRVI 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CHROMATIUM VINO SUM 189-373 CH60_MYCTU 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(65 KD ANTIGEN)HEAT 191-375 CH60_NEIME 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(63 KD STRESS PROTEIN 189-373 CH60_TREPA 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(TPN60)(TP4 ANTIGEN) 190-374 CH60_HELPY 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(HEAT SHOCK PROTEIN 6 191-375 CH60_NEIGO 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(63 KD STRESS PROTEIN) 222-406 CH61_CUCMA MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR; CUCURBITA MAXIMA (PUMPKI 189-373 CH60_MYCPA 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(65 KD ANTIGEN)HEAT 230-414 MPU15989 MPU15989 NID:g559802; Mycobacterium paratuberculosis 224-408 S26582 chaperonin hsp60; maize 191-375 S40247 heat-shock protein; Neisseria gonorrhoeae 189-373 CH60_CLOAB 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); CLOSTRIDIUM ACETOB 191-375 CH60_NEIFL 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(63 KD STRESS PROTEIN 190-373 CH60_LEGPN 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(58 KD COMMON ANTIGEN) 222-406 CH62_CUCMA MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR; CUCURBITA MAXIMA (PUMPKI 191-375 CHTGROESL1 CHTGROESL NID: g402332; Chlamydia trachomatis DNA 64-248 S40172 S40172 NID: g251679; Chlamydia psittaci pigeon strain P-1041 189-373 SYOGROEL2 SYOGROEL2 NID:g562270; Synechococcus vulgaris DNA 191-375 CH60_CHLPS 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(57 KD CHLAMYDIAL HYP) 188-372 CH62_STRAL 60 KD CHAPERONIN 2 (PROTEIN CPN60 2)(GROEL PROTEIN 2)(HSP56); STRE 189-373 CH62_MYCLE 60 KD CHAPERONIN 2 (PROTEIN CPN60 2)(GROEL PROTEIN 2)(65 KD ANTIGEN) 236-420 MSGANTM MSGANTM NID: g149923; M.leprae DNA, clone Y3178 CPN60 PRECURSOR; BRASSICA NAPUS (RAPE) 105-289 PMSARG2 PMSARG2 NID: g607157; Prochlorococcus marinus 234-417 RUB2_BRANA RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERO 75-259 CRECPN1A

CRECPN1A NID: g603910; Chlamydomonas reinhardtii cDNA to mRNA 215-400 P60_CRIGR MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)(CH224-408 CRECPN1B CRECPN1B NID: g603912; Chlamydomonas reinhardtii cDNA to mRNA 191-375 RUBA_WHEAT RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERO 189-373 B47292 heat shock protein groEL; Mycobacterium tuberculosis 206-391 CELHSP60CP CELHSP60CP NID: g533166; Caenorhabditis elegans (strain CB1392) cDNA 215-400 P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)(CH 215-400 P60_MOUSE MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)(CH 215-400 P60_RAT MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN)(CH 215-400 A41931) chaperonin hsp60; mouse 197-382 MMHSP60A MMHSP60A NID:g51451; house mouse 218-402 CH63_HELV 63 KD CHAPERONIN PRECURSOR (P63); HELIOTHIS VIRESSENS (NOCTUID MOTH) 205-390 EGHSP60GN EGHSP60GN NID: g1217625; Euglena gracilis. 222-407 HS60_SCHPO PROBABLE HEAT SHOCK PROTEIN 60 PRECURSOR; SCHIZOSACCHAROMYCES POMBE 198-385 S61295 heat shock protein 60; Trypanosoma cruzi 198-385 TRBMTHSP TRBMTHSP NID: g903883; Mitochondrion Trypanosoma brucei (strain EATRO 8-69 ECOGROELA ECOGROELA NID: g146268; E.coli DNA, clone E. 142-325 ENHCPN60P ENHCPN60P NID: g675513; Entamoeba histolytica (strain HM-1:IMSS) DNA 257-433 CH60_PLAFG MITOCHONDRIAL CHAPERONIN CPN60 PRECURSOR; PLASMODIUM FALCIPARUM (ISO 1-90 CRECPN1C CRECPN1C NID: g603914; Chlamydomonas reinhardtii cDNA to mRNA; 5-65 ATTS0779 ATTS0779 NID: g17503; thale cress 189-373 CH60_MYCGE 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN); MYCOPLASMA GENITAL 228-411 HTOHSP60X HTOHSP60X NID: g553068; Histoplasma capsulatum (strain G217B) DNA 190-297 CH60_SYNPN6 60 KD CHAPERONIN (PROTEIN CPN60)(GROEL PROTEIN)(FRAGMENT); and SYNECHO 169-245 RUBA_ARATH RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD CHAPERONIN ALPHA).

54. (New) A monomeric polypeptide having chaperone activity and incapable of multimerisation characterised in that in the absence of ATP the polypeptide has a protein refolding activity of more than 50%, said refolding activity being determined by contacting the

polypeptide with an inactivated protein of known specific activity prior to inactivation, and then determining the specific activity of the said protein after contact with the polypeptide, the % refolding activity being:

$$\frac{\text{specific activity of protein after contact with polypeptide} \times 100}{\text{specific activity of protein prior to inactivation}} \quad 1$$

wherein the selected amino acid is selected from the group consisting of 230-271, 191-345, 191-376, 193-335 and 193-337 of GroEL and a corresponding sequence of a chaperonin protein selected from the group consisting of:

CH60_ECOLI_190; CH60_SALTI_190; S56371_191; CH60_LEPIN_190; S47530_191;
LPNHTPBG_190; CH60_ACTAC_189; JC4519_191 ; CH60_BRUAB_191;
CH60_HAEIN_191; CH60_CAUCR_190; CH60_AMOPS_190; CH60_HAEDU_191;
CH61_RHIME_191; CH60_LEGMI_190; CH60_YEREN_191; CH63_BRAJA_190;
CH60_PORGI_191; S52901_191; S26423_191 ; RSU373691_191; CH62_BRAJA_190;
CH60_ACYPS_191; CH63_RHIME_191; YEPHSPCRP1_191; CH60_BORPE_191;
BRUGRO1_189; CH60_PSEAE_191; CH60_BARBA_190; BAOBB63A_191;
CH60_BACST_189; CH60_BACSU_188; CH60_AGRTU_191; B36917_191 ; PAU17072_191;
CH60_RHILV_191; CH61_STRCO_187; CH60_COXBU_191; CH62_RHIME_191;
PSEGROESL1_191; CH61_SYNYY3_189; CH60_CLOTM_189; CH60_PSEPU_191;
CH60_SYNTP7_190; CH60_GALSU_190; CH60_ZYMMO_190; JC2564_191;
CH60_CHRVI_191; CH60_MYCTU_189; CH60_NEIME_191; CH60_TREPA_189;
CH60_HELPY_190; CH60_NEIGO_191; CH61_CUCMA_222; CH60_MYCPA_189;
MPU15989_230 ; S26582_224 ; S40247_191 ; CH60_CLOAB_189; CH60_NEIFL_191;
CH60_LEGPN_190; CH62_CUCMA_222; CHTGROESL1_191; S40172_64 ;
SYOGROEL2_189 ; CH60_CHLPS_191; CH62_STRAL_188; CH62_MYCLE_189;
MSGANTM_236; CH60_BORBU_190; S26583_224; A49209_190; MZECPN60B_224;
CH60_THEP3_189; CH60_STAEP_188; CH60_LACLA_189; CH61_STRAL_188;
CH60_CHLPN_191; MZECPN60A_224; HECHSPAB1_190; CH60_ARATH_221;
CH60_MAIZE_224; CH60_CHLTR_190; CH60_STAAU_189; CH60_CLOPE_189;
HS60_YEAST_212; CH60_PYRSA_217; CH60_EHRCH_191; CHTGROE1_191;
CH60_THETH_188; TAU294831_189; CH60_RICTS_190; SYCCPNC_189; CPU308211_190;
CH61_MYCLE_189; PSU21139_239; CH60_COWRU_191; RUBB_BRANA_245;

PATENT
674508-2001

SCCPN60_144; CH60_EHRRI_153; RUBB_ARATH_245; ATU49357_235;
RUB1_BRANA_195; CH62_SYN3_189; RUBA_RICCO_178; CH60_ODOSI_190;
PSU21105_236; CH60_BRANA_224; PMSARG2_105; RUB2_BRANA_234; CRECPN1A_75;
P60_CRIGR_215; CRECPN1B_224; RUBA_WHEAT_191; B47292_189; CELHSP60CP_206;
P60_HUMAN_215; P60_MOUSE_215; P60_RAT_215; A41931_215; MMHSP60A_197;
CH63_HELVI_218; EGHSP60GN_205; HS60_SCHPO_222; S61295_198; TRBMTHSP_198;
ENHCPN60P_142; CH60_PLAFG_257; CH60_MYCGE_189 and HTOHSP60X_228.
